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PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * *   Welcome to STN International   * * * * * * * * * *

NEWS 1   Web Page URLs for STN Seminar Schedule - N. America
NEWS 2   "Ask CAS" for self-help around the clock
NEWS 3 SEP 01   New pricing for the Save Answers for SciFinder Wizard within
                  STN Express with Discover!
NEWS 4 OCT 28   KOREAPAT now available on STN
NEWS 5 NOV 30   PHAR reloaded with additional data
NEWS 6 DEC 01   LISA now available on STN
NEWS 7 DEC 09   12 databases to be removed from STN on December 31, 2004
NEWS 8 DEC 15   MEDLINE update schedule for December 2004
NEWS 9 DEC 17   ELCOM reloaded; updating to resume; current-awareness
                  alerts (SDIs) affected
NEWS 10 DEC 17   COMPUAB reloaded; updating to resume; current-awareness
                  alerts (SDIs) affected
NEWS 11 DEC 17   SOLIDSTATE reloaded; updating to resume; current-awareness
                  alerts (SDIs) affected
NEWS 12 DEC 17   CERAB reloaded; updating to resume; current-awareness
                  alerts (SDIs) affected
NEWS 13 DEC 17   THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
NEWS 14 DEC 30   EPFULL: New patent full text database to be available on STN
NEWS 15 DEC 30   CAPLUS - PATENT COVERAGE EXPANDED
NEWS 16 JAN 03   No connect-hour charges in EPFULL during January and
                  February 2005
NEWS 17 FEB 25   CA/CAPLUS - Russian Agency for Patents and Trademarks
                  (ROSPATENT) added to list of core patent offices covered
NEWS 18 FEB 10   STN Patent Forums to be held in March 2005
NEWS 19 FEB 16   STN User Update to be held in conjunction with the 229th ACS
                  National Meeting on March 13, 2005
NEWS 20 FEB 28   PATDPAFULL - New display fields provide for legal status
                  data from INPADOC
NEWS 21 FEB 28   BABS - Current-awareness alerts (SDIs) available
NEWS 22 FEB 28   MEDLINE/LMEDLINE reloaded
NEWS 23 MAR 02   GBFULL: New full-text patent database on STN
NEWS 24 MAR 03   REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS 25 MAR 03   MEDLINE file segment of TOXCENTER reloaded

NEWS EXPRESS   JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

NEWS HOURS   STN Operating Hours Plus Help Desk Availability
NEWS INTER   General Internet Information
NEWS LOGIN   Welcome Banner and News Items
NEWS PHONE   Direct Dial and Telecommunication Network Access to STN
NEWS WWW   CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

```
L3      ANSWER 1 OF 1   CAPLUS   COPYRIGHT 2005 ACS on STN
AN      1997:63969  CAPLUS
DN      126:85511
TI      Isolation of 5'-untranslational region of trout Cyp1A1 gene
AU      Roh, Yong Nam; Sheen, Yhun Yhong
CS      College of Pharmacy, Ewha Woman's University, Seoul, 120-750, S. Korea
SO      Archives of Pharmacal Research (1996), 19(6), 450-455
        CODEN: APHRDQ; ISSN: 0253-6269
PB      Pharmaceutical Society of Korea
DT      Journal
LA      English
RE.CNT  19     THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> s l1 and exonuclease
L4              15 L1 AND EXONUCLEASE

=> s l4 and nuclease
L5               5 L4 AND NUCLEASE

=> d l5 1-5

L5      ANSWER 1 OF 5   BIOSIS   COPYRIGHT (c) 2005 The Thomson Corporation  on STN
AN      1992:454576  BIOSIS
DN      PREV199294095976; BA94:95976
TI      CDNA CLONING SEQUENCING EXPRESSION AND POSSIBLE DOMAIN STRUCTURE OF HUMAN
        APEX NUCLEASE HOMOLOGOUS TO ESCHERICHIA-COLI EXONUCLEASE
        III.
AU      SEKI S [Reprint author]; HATSUSHIKA M; WATANABE S; AKIYAMA K; NAGAO K;
        TSUTSUI K
CS      DEP MOL BIOL, INST CELLULAR MOL BIOL, OKAYAMA UNIV MED SCH, 2-5-1
        SHIKATA-CHO, OKAYAMA 700, JPN
SO      Biochimica et Biophysica Acta, (1992) Vol. 1131, No. 3, pp. 287-299.
        CODEN: BBACAQ. ISSN: 0006-3002.
DT      Article
FS      BA
LA      ENGLISH
ED      Entered STN: 7 Oct 1992
        Last Updated on STN: 8 Oct 1992


L5      ANSWER 2 OF 5   EMBASE   COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
        on STN
AN      92231583  EMBASE
DN      1992231583
TI      cDNA cloning, sequencing, expression and possible domain structure of
        human APEX nuclease homologous to Escherichia coli
        exonuclease III.
AU      Seki S.; Hatsushika M.; Watanabe S.; Akiyama K.; Nagao K.; Tsutsui K.
CS      Department of Molecular Biology, Inst. of Cellular/Molecular Biology,
        Okayama University Medical School, 2-5-1, Shikata-cho,Okayama 700, Japan
SO      Biochimica et Biophysica Acta - Gene Structure and Expression, (1992)
        1131/3 (287-299).
        ISSN: 0167-4781  CODEN: BBGSD5
CY      Netherlands
DT      Journal; Article
FS      029      Clinical Biochemistry
LA      English
SL      English

L5      ANSWER 3 OF 5      MEDLINE on STN
AN      92329542      MEDLINE
DN      PubMed ID: 1627644
TI      cDNA cloning, sequencing, expression and possible domain structure of
        human APEX nuclease homologous to Escherichia coli
        exonuclease III.
AU      Seki S; Hatsushika M; Watanabe S; Akiyama K; Nagao K; Tsutsui K
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* * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 15:14:17 ON 10 MAR 2005

=> FIL MEDLINE
COST IN U.S. DOLLARS                           SINCE FILE      TOTAL
                                                 ENTRY        SESSION
FULL ESTIMATED COST                              0.21          0.21

FILE 'MEDLINE' ENTERED AT 15:14:43 ON 10 MAR 2005

 FILE LAST UPDATED: 9 MAR 2005 (20050309/UP).  FILE COVERS 1950 TO DATE.

 On December 19, 2004, the 2005 MeSH terms were loaded.

 The MEDLINE reload for 2005 is now available.  For details enter HELP
 RLOAD at an arrow promt (=>).  See also:

     http://www.nlm.nih.gov/mesh/
     http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html

 OLDMEDLINE now back to 1950.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2005 vocabulary.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

=> E HENIKOFF S/AU 25
E1         8      HENIKOFF L M/AU
E2         1      HENIKOFF L M JR/AU
E3       132 --> HENIKOFF S/AU
E4        40      HENIKOFF STEVEN/AU
E5         1      HENIN/AU
E6         4      HENIN A/AU
E7         4      HENIN AUDE/AU
E8         1      HENIN B/AU
E9         3      HENIN C/AU
E10      157      HENIN D/AU
E11       18      HENIN DOMINIQUE/AU
E12        1      HENIN E/AU
E13       33      HENIN F/AU
E14        2      HENIN FRANCOISE/AU
E15        1      HENIN GUERIN C/AU
E16       18      HENIN J/AU
E17       18      HENIN J M/AU
E18        5      HENIN J P/AU
E19        1      HENIN JEROME/AU
E20        1      HENIN LANDES D/AU
E21        3      HENIN M/AU
E22        1      HENIN M D/AU
E23        1      HENIN MARTA/AU
E24       15      HENIN N/AU
E25        4      HENIN O/AU

=> S (E3) AND 1980<=PY<=1998
           132 "HENIKOFF S"/AU
       6884261 1980<=PY<=1998
L1          95 ("HENIKOFF S"/AU) AND 1980<=PY<=1998

=> S (E3) AND 1980<=PY<=1998 AND (EXONUCLEASE III)
           132 "HENIKOFF S"/AU
       6884261 1980<=PY<=1998
          3917 EXONUCLEASE
          1704 EXONUCLEASES
          4766 EXONUCLEASE
                  (EXONUCLEASE OR EXONUCLEASES)
```

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       220819 III
          167 IIIS
       220908 III
              (III OR IIIS)
          698 EXONUCLEASE III
              (EXONUCLEASE(W)III)
L2            6 ("HENIKOFF S"/AU) AND 1980<=PY<=1998 AND (EXONUCLEASE III)
```

=> DIS L2 1- TI
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):Y

L2   ANSWER 1 OF 6   MEDLINE on STN
TI   Ordered deletions using **exonuclease III.**

L2   ANSWER 2 OF 6   MEDLINE on STN
TI   Ordered deletions using **exonuclease III.**

L2   ANSWER 3 OF 6   MEDLINE on STN
TI   Ordered deletions using **exonuclease III.**

L2   ANSWER 4 OF 6   MEDLINE on STN
TI   Ordered deletions for DNA sequencing and in vitro mutagenesis by
      polymerase extension and **exonuclease III** gapping of
      circular templates.

L2   ANSWER 5 OF 6   MEDLINE on STN
TI   Unidirectional digestion with **exonuclease III** in DNA
      sequence analysis.

L2   ANSWER 6 OF 6   MEDLINE on STN
TI   Unidirectional digestion with **exonuclease III** creates
      targeted breakpoints for DNA sequencing.

=> DIS L2 1- IBIB ABS
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):Y
THE ESTIMATED COST FOR THIS REQUEST IS 1.32 U.S. DOLLARS
DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:Y

L2   ANSWER 1 OF 6   MEDLINE on STN
ACCESSION NUMBER: 97002661   MEDLINE
DOCUMENT NUMBER: PubMed ID: 8850001
TITLE: Ordered deletions using **exonuclease III**
                     .
AUTHOR: Clark D; **Henikoff S**
CORPORATE SOURCE: Fred Hutchinson Cancer Research Center, Howard Hughes
                     Medical Institute, Seattle, WA, USA.
SOURCE: Methods in molecular biology (Clifton, N.J.),
                     (1996) 57 139-47. Ref: 7
                     Journal code: 9214969. ISSN: 1064-3745.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
                     General Review; (REVIEW)
                     (REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
                     Last Updated on STN: 19970128
                     Entered Medline: 19961210

L2   ANSWER 2 OF 6   MEDLINE on STN
ACCESSION NUMBER: 96281045   MEDLINE
DOCUMENT NUMBER: PubMed ID: 8713883
TITLE: Ordered deletions using **exonuclease III**
                     .
AUTHOR: Clark D; **Henikoff S**
CORPORATE SOURCE: Department of Biology, University of New Brunswick,
                     Fredericton, Canada.

TITLE: Ordered deletions using **exonuclease III**
                     .
AUTHOR: Clark D; **Henikoff S**
CORPORATE SOURCE: Basic Sciences Division, Fred Hutchinson Cancer Research
                     Center, Seattle, WA.

TITLE: Ordered deletions for DNA sequencing and in vitro
                     mutagenesis by polymerase extension and **exonuclease
                     III** gapping of circular templates.
AUTHOR: **Henikoff S**
CORPORATE SOURCE: Fred Hutchinson Cancer Research Center, Seattle, WA 98104.
CONTRACT NUMBER: GM29009 (NIGMS)
AB   A simple method is described for generating nested deletions from any
     fixed point in a cloned inset. Starting with a single-stranded phagemid
     template, T4 DNA polymerase is used to extend an annealed primer. This
     leads to a fully double-stranded circular molecule with a nick or small
     gap just 5' to the primer. **Exonuclease III** initiates
     progressive digestion from the resulting 3' end. Removal of timed
     aliquots and digestion with a single-strand specific endonuclease leads to
     a series of linear nested fragments having a common end corresponding to
     the 5' end of the primer. These molecules are circularized and used to
     transform cells, providing large numbers of deletion clones with targeted
     breakpoints. The 6-step procedure involves successive additions to tubes,
     beginning with a single-stranded template and ending with transformation;
     no extractions, precipitations or centrifugations are needed. Results are
     comparable to those obtained with standard **Exonuclease
     III**-generated deletion protocols, but there is no requirement for

restriction endonuclease digestion or for highly purified double-stranded
DNA starting material. This procedure provides a strategy for obtaining
nested deletions in either direction both for DNA sequencing and for
functional analysis.

L2   ANSWER 5 OF 6   MEDLINE on STN
ACCESSION NUMBER: 88121636   MEDLINE
DOCUMENT NUMBER: PubMed ID: 3323819
TITLE: Unidirectional digestion with **exonuclease**
                     III in DNA sequence analysis.
AUTHOR: **Henikoff S**
SOURCE: Methods in enzymology, **(1987)** 155 156-65.
                     Journal code: 0212271. ISSN: 0076-6879.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198803
ENTRY DATE: Entered STN: 19900308
                     Last Updated on STN: 19900308
                     Entered Medline: 19880318

L2   ANSWER 6 OF 6   MEDLINE on STN
ACCESSION NUMBER: 84262487   MEDLINE
DOCUMENT NUMBER: PubMed ID: 6235151
TITLE: Unidirectional digestion with **exonuclease**
                     III creates targeted breakpoints for DNA
                     sequencing.
AUTHOR: **Henikoff S**
CONTRACT NUMBER: GM29009 (NIGMS)
SOURCE: Gene, **(1984 Jun)** 28 (3) 351-9.
                     Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J02527; GENBANK-K02461; GENBANK-X06286;
                     GENBANK-Y00606
ENTRY MONTH: 198409
ENTRY DATE: Entered STN: 19900320
                     Last Updated on STN: 19970203
                     Entered Medline: 19840919
AB   A method is described for the rapid generation and cloning of deletion
     derivatives well-suited for the sequencing of long stretches of DNA. This
     method is based on two useful features of **exonuclease**
     III: (1) processive digestion at a very uniform rate and (2)
     failure to initiate digestion at DNA ends with four-base 3'-protrusions.
     The method was applied to a 4570-bp Drosophila genomic DNA fragment cloned
     in the single-stranded phage vector M 13mp18. An ordered set of deletion
     clones was made by first cutting replicative form(RF) DNA with two
     restriction enzymes in the polylinker region of the vector between the
     Drosophila DNA and the sequencing primer binding site. One enzyme left a
     four-base 3'-protrusion that protected the remainder of the vector from
     exonuclease III attack, allowing unidirectional
     digestion of the insert sequence from the 5'-protruding end left by the
     other enzyme. Aliquots were removed at uniform intervals, treated with S1
     nuclease, Klenow DNA polymerase, T4 DNA ligase, and then used to transfect
     competent cells. Most of the resulting clones derived from each aliquot
     were deleted to a predicted extent with only slight scatter, even for
     deletions of more than 4 kb. The method permits efficient isolation of
     clusters of deletion breakpoints within small preselected regions of large
     DNA segments, allowing nonrandom sequence analysis.

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---Logging off of STN---